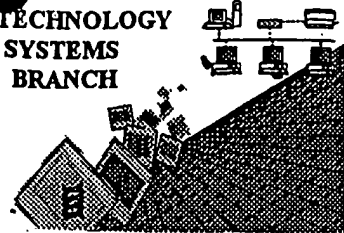MAIL THIS COPY WITH 916 NOTICE

BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/914,454 A_

Source: _PCTO9_

Date Processed by STIC: _6/12/02_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
          Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>   <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/914,454_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
      Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                            prevent "wrapping."

2_____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_✓_Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
      Numbering   use space characters, instead.

4_____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                            ensure your subsequent submission is saved in ASCII text.

5_____Variable Length   Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                            each n or Xaa can only represent a single residue. Please present the maximum number of each
                            residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
      "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                            previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                            the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                            Artificial or Unknown sequences.

7_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
      (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                            (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                            (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                            This sequence is intentionally skipped

                            Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
      (NEW RULES)   <210> sequence id number
                            <400> sequence id number
                            000

9_____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
      (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                            In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
       Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                            is Artificial Sequence

11_____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                            Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                            "Unknown." Please explain source of genetic material in <220> to <223> section.
                            (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
       "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                            listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n   n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent
                            any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

PCT0

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/914,454A

DATE: 07/05/2002
TIME: 15:39:27

Does Not Comply Corrected Diskette Needed (handwritten stamp)

Input Set : N:\Crf3\06122002\I914454.raw
Output Set: N:\CRF3\07052002\I914454A.raw

```
      1  <110> APPLICANT: Chiron SpA              → delete multiple,
W-->  2  <110> APPLICANT: GRANDI Guido
W-->  3  <110> APPLICANT: RAPPUOLI Rino            <110's only one is ne
W-->  4  <110> APPLICANT: GIULIANI Marzia Monica
W-->  5  <110> APPLICANT: PIZZA Mariagrazia
      6  <120> TITLE OF INVENTION: ENHANCEMENT OF BACTERICIDAL ACTIVITY OF NEISSERIA ANTIGENS
WITH
      7        OLIGONUCLEOTIDES CONTAINING CG MOTIFS
      8  <130> FILE REFERENCE: P023888WO
      9  <140> CURRENT APPLICATION NUMBER: US/09/914,454A
     10  <141> CURRENT FILING DATE: 2002-03-22
     11  <150> PRIOR APPLICATION NUMBER: US-60/121,792
W--> 12  <151> PRIOR FILING DATE: 26/02/1999   1999-02-26 ⟵ use this format
     13  <160> NUMBER OF SEQ ID NOS: 34                              dates
     14  <170> SOFTWARE: SeqWin99
```

ERRORED SEQUENCES

```
    304  <210> SEQ ID NO: 31
    305  <211> LENGTH: 442   441 shown (p. 2)
    306  <212> TYPE: PRT
    307  <213> ORGANISM: Neisseria meningitidis
    308  <400> SEQUENCE: 31
    309        Met Lys Lys Tyr Leu Phe Arg Ala Ala Leu Tyr Gly Ile Ala Ala Ala
    310        1               5                   10                  15
    311        Ile Leu Ala Ala Cys Gln Ser Lys Ser Ile Gln Thr Phe Pro Gln Pro
    312                    20                  25                  30
    313        Asp Thr Ser Val Ile Asn Gly Pro Asp Arg Pro Val Gly Ile Pro Asp
    314                    35                  40                  45
    315        Pro Ala Gly Thr Thr Val Gly Gly Gly Gly Ala Val Tyr Thr Val Val
    316            50                  55                  60
    317        Pro His Leu Ser Leu Pro His Trp Ala Ala Gln Asp Phe Ala Lys Ser
    318        65                  70                  75                  80
    319        Leu Gln Ser Phe Arg Leu Gly Cys Ala Asn Leu Lys Asn Arg Gln Gly
    320                        85                  90                  95
    321        Trp Gln Asp Val Cys Ala Gln Ala Phe Gln Thr Pro Val His Ser Phe
    322                    100                 105                 110
    323        Gln Ala Lys Gln Phe Phe Glu Arg Tyr Phe Thr Pro Trp Gln Val Ala
    324                    115                 120                 125
    325        Gly Asn Gly Ser Leu Ala Gly Thr Val Thr Gly Tyr Tyr Glu Pro Val
    326                    130                 135                 140
    327        Leu Lys Gly Asp Asp Arg Arg Thr Ala Gln Ala Arg Phe Pro Ile Tyr
    328        145                 150                 155                 160
```

RAW SEQUENCE LISTING   DATE: 07/05/2002
PATENT APPLICATION: US/09/914,454A   TIME: 15:39:27

Input Set : N:\Crf3\06122002\I914454.raw
Output Set: N:\CRF3\07052002\I914454A.raw

```
329    Gly Ile Pro Asp Asp Phe Ile Ser Val Pro Leu Pro Ala Gly Leu Arg
330                    165             170             175
331    Ser Gly Lys Ala Leu Val Arg Ile Arg Gln Thr Gly Lys Asn Ser Gly
332                    180             185             190
333    Thr Ile Asp Asn Thr Gly Gly Thr His Thr Ala Asp Leu Ser Arg Phe
334                    195             200             205
335    Pro Ile Thr Ala Arg Thr Thr Ala Ile Lys Gly Arg Phe Glu Gly Ser
336            210             215             220
337    Arg Phe Leu Pro Tyr His Thr Arg Asn Gln Ile Asn Gly Gly Ala Leu
338    225             230             235             240
339    Asp Gly Lys Ala Pro Ile Leu Gly Tyr Ala Glu Asp Pro Val Glu Leu
340                    245             250             255
341    Phe Phe Met His Ile Gln Gly Ser Gly Arg Leu Lys Thr Pro Ser Gly
342            260             265             270
343    Lys Tyr Ile Arg Ile Gly Tyr Ala Asp Lys Asn Glu His Pro Tyr Val
344            275             280             285
345    Ser Ile Gly Arg Tyr Met Ala Asp Lys Gly Tyr Leu Lys Leu Gly Gln
346            290             295             300
347    Thr Ser Met Gln Gly Ile Lys Ser Tyr Met Arg Gln Asn Pro Gln Arg
348    305             310             315             320
349    Leu Ala Glu Val Leu Gly Gln Asn Pro Ser Tyr Ile Phe Phe Arg Glu
350                    325             330             335
351    Leu Ala Gly Ser Ser Asn Asp Gly Pro Val Gly Ala Leu Gly Thr Pro
352                    340             345             350
353    Leu Met Gly Glu Tyr Ala Gly Ala Val Asp Arg His Tyr Ile Thr Leu
354            355             360             365
355    Gly Ala Pro Leu Phe Val Ala Thr Ala His Pro Val Thr Arg Lys Ala
356    370             375             380
357    Leu Asn Arg Leu Ile Met Ala Gln Asp Thr Gly Ser Ala Ile Asp Gly
358    385             390             395             400
359    Ala Val Arg Val Asp Tyr Phe Trp Gly Tyr Gly Asp Glu Ala Gly Glu
360                    405             410             415
361    Leu Ala Gly Lys Gln Lys Thr Thr Gly Tyr Val Trp Gln Leu Leu
362                    420             425             430
363    Pro Asn Gly Met Lys Pro Glu Tyr Arg Pro
364            ~~435~~ 435          ~~440~~ 440
```

E--> 364

misaligned amino acid numbering — see item 3 on Error Summary Sheet

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/05/2002
PATENT APPLICATION: US/09/914,454A   TIME: 15:39:28

Input Set : N:\Crf3\06122002\I914454.raw
Output Set: N:\CRF3\07052002\I914454A.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

VERIFICATION SUMMARY   DATE: 07/05/2002
PATENT APPLICATION: US/09/914,454A   TIME: 15:39:28

Input Set : N:\Crf3\06122002\I914454.raw
Output Set: N:\CRF3\07052002\I914454A.raw

L:2 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:3 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:4 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:5 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:12 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:364 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
L:364 M:252 E: No. of Seq. differs, <211> LENGTH:Input:442 Found:441 SEQ:31